Amino Acid Inspector

This inspector allows you to manipulate proteins created or filtered through Alchemy. When you first select this inspector, all amino acids in the current molecule will be located AND IDENTIFIED. The identification is done by counting atoms of various types in the sidechain and checking the bonds to resolve ambiguities. Only 20 of the most common amino acids are currently supported. If you use an exotic amino acid, it may be mis-identified. Also, proline is currently not identified correctly. Amino acids are sorted so the N terminus appears first.

Once the amino acids have been identified, you can modify their dihedral angles. First select one or more residues, then use the sliders or text displays to change their angles. Changes will be shown in the molecule view in real time.

A button is also provided to transfer the amino acid sequence to the Protein Tool for analysis. You need to open the protein tool manually to

use this.